

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2005, 15:22:21 ; Search time 177 Seconds
(without alignments)
167.800 Million cell updates/sec

Title: US-10-617-978-20
Perfect score: 343
Sequence: 1 ADVPGNYPLDSSDNTYLCA.....GYCYAFQWCFLKDNVYK 58

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	222	64.7	58	1 BIRT PARTR	P58752 parathus
2	188	54.8	80	2 Q6WJF5	Q6WJF5 mesobuthus
3	127	37.0	67	1 SCXC_CENNO	P63019 centruride
4	123	35.9	64	2 Q6V4Y9	Q6V4Y9 centruride
5	119.5	34.8	65	1 SCXM_CENSC	P56646 centruride
6	117	34.1	64	2 Q6V4Y8	Q6V4Y8 centruride
7	117	34.1	87	1 SCX2_CENSC	P01494 centruride
8	117	34.1	87	1 SCX3_CENSC	P01494 centruride
9	116	33.8	64	2 Q6V4Y0	Q6V4Y0 centruride
10	116	33.8	64	2 Q6V4Y4	Q6V4Y4 centruride
11	115	33.5	64	2 Q6V4Y7	Q6V4Y7 centruride
12	115	33.5	73	2 Q68PG2	Q68PG2 centruride
13	115	33.5	85	1 SCX7_CENLL	P59865 centruride
14	113	32.9	66	2 Q68PG4	Q68PG4 centruride
15	113	32.9	67	2 Q68PG7	Q68PG7 centruride
16	113	32.9	87	1 SCXB_CENLL	P72167 centruride
17	111	32.4	87	1 SCXB_CENNO	P45663 centruride
18	110	32.1	66	1 SCX2_CENSU	P08900 centruride
19	110	32.1	87	1 -SCX3_CENSC	Q95wd2 centruride
20	109	31.8	64	2 Q6V4Y3	Q6V4Y3 centruride
21	109	31.8	66	1 SCX7_CENLL	P45667 centruride
22	109	31.8	87	1 SCXX_CENNO	P45664 centruride
23	108	31.5	62	1 SCX8_CENNO	Q9tw10 centruride
24	108	31.5	66	1 SCX2_CENLL	P59898 centruride
25	108	31.5	84	1 SCX2_CENNO	P01495 centruride
26	107	31.2	64	2 Q6V4Y1	Q6V4Y1 centruride
27	107	31.2	64	2 Q6V4Y2	Q6V4Y2 centruride
28	107	31.2	64	2 Q6V4Y6	Q6V4Y6 centruride
29	107	31.2	66	1 SCX1_CENII	P59897 centruride
30	107	31.2	66	1 SCX1_CENLI	P18926 centruride
31	107	31.2	66	1 SCX1_CENLL	P45666 centruride

32	107	31.2	85	1 SCCE_CENLL	Q721k6 centruride
33	107	31.2	87	1 SC2B_CENLL	P59899 centruride
34	107	31.2	87	1 SCX4_CENNO	P45662 centruride
35	107	31.2	87	1 SCXC_CENLL	Q7yt61 centruride
36	106.5	31.0	87	1 SCX1_CENSC	P01492 centruride
37	106	30.9	64	2 Q6V4Y5	Q6v4y5 centruride
38	106	30.9	69	2 Q68PG9	Q68pg9 centruride
39	106	30.9	69	2 Q68PH2	Q68ph2 centruride
40	106	30.9	85	1 SCX6_CENLL	Q721k5 centruride
41	106	30.9	87	2 Q68PH1	Q68ph1 centruride
42	105	30.6	69	2 Q68PG8	Q68pg8 centruride
43	105	30.6	69	2 Q68PH0	Q68ph0 centruride
44	105	30.6	87	2 Q68PH3	Q68ph3 centruride
45	105	30.6	87	2 Q68PH4	Q68ph4 centruride

ALIGNMENTS

RESULT 1

ID BIRT PARTR STANDARD; PRT; 58 AA.
AC P58752;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Birtoxin.
OS Parabuthus transvaalicus (South African fattail scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthida; Buthoidea; Buthidae; Parabuthus.
OX NCBI_TaxID=170972;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=21518524; PubMed=11606203;
RA Inceoglu B., Lango J., Wu J., Hawkins P., Southern J., Hammock B.D.;
RT "Isolation and characterization of a novel type of neurotoxic peptide
from the venom of the South African scorpion Parabuthus transvaalicus
(Buthidae).";
RL Eur. J. Biochem. 268:5407-5413(2001).
CC -1- FUNCTION: Binds to sodium channels and inhibits the inactivation
of the activated channels, thereby blocking neuronal transmission
(By similarity). Moderately toxic, but very high abundant. Lethal
to mice. Do not target reptilian channels.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
DR HSP; P41964; IMYN.
DR InterPro; IPR002061; Scorpion_toxinL.
DR Pfam; PF00537; Toxin_3; 1.
DR ProDom; PD000908; Scorpion_toxinL; 1.
KW Direct protein sequencing; Ionic channel inhibitor; Neurotoxin;
FT DISULFID 18 41 By similarity.
FT DISULFID 27 46 By similarity.
FT DISULFID 31 48 By similarity.
SQ SEQUENCE 58 AA; 6548 MW; F5C9EA421959D096 CRC64;

Query Match 64.7%; Score 222; DB 1; Length 58;

Best Local Similarity 60.3%; Pred. No. 2.4e-18;

Matches 35; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 ADVPGNYPLDSSDNTYLCAPLGNDPCIKIKGKGVYGYCYAFQWCFLKDNVYK 58

Db 1 ADVPGNYPLDKGNTYKFLGLGNEBCLNCKLHGVQYCYASKCWCYLEDDKDSV 58

RESULT 2

Q6WJF5
ID Q6WJF5 PRELIMINARY; PRT; 80 AA.
AC Q6WJF5;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)